

What is claimed is:

1. A gene encoding the following protein (a), (b), or (c):

(a) a protein consisting of the amino acid sequence as shown in SEQ ID NO: 2 in the Sequence Listing;

(b) a protein consisting of an amino acid sequence derived from the amino acid sequence as shown in SEQ ID NO: 2 in the Sequence Listing by deletion, substitution, or addition of one or several amino acid residues and having activity of imparting salt stress tolerance to plants; or

(c) a protein consisting of an amino acid sequence derived from the amino acid sequence as shown in SEQ ID NO: 2 in the Sequence Listing by deletion, substitution, or addition of one or several amino acid residues and having UDP-glucose 4-epimerase activity.

2. A gene consisting of the following DNA (d), (e), or (f):

(d) DNA consisting of the nucleotide sequence as shown in SEQ ID NO: 1 in the Sequence Listing;

(e) DNA hybridizing under stringent conditions to DNA consisting of a nucleotide sequence complementary to DNA consisting of the nucleotide sequence as shown in SEQ ID NO: 1 in the Sequence Listing and encoding a protein having activity of imparting salt stress tolerance to plants; or

(f) DNA hybridizing under stringent conditions to DNA consisting of a nucleotide sequence complementary to DNA consisting of the nucleotide sequence as shown in SEQ ID NO: 1 in the Sequence Listing and encoding a protein having UDP-glucose 4-epimerase activity.

3. A recombinant vector comprising the gene according to claim 1 or 2.

4. A transgenic plant into which the gene according to claim 1 or 2 or the recombinant vector according to claim 3 has been introduced.

5. A salt stress tolerant transgenic plant into which the gene according to claim 1 or 2 or the recombinant vector according to claim 3 has been introduced.

6. The transgenic plant according to claim 4 or 5, wherein the plant is monocotyledonous.

7. The transgenic plant according to claim 6, wherein the monocotyledonous plant belongs to the family *Gramineae*, *Liliaceae*, or *Zingiberaceae*.

8. The transgenic plant according to claim 7, wherein the plant that belongs to the family *Gramineae* is selected from the group consisting of rice, barley, wheat, maize, sugarcane, *Zoysia*, sorghum, Italian millet, and Japanese millet.

9. The transgenic plant according to claim 4 or 5, wherein the plant is dicotyledonous.

10. The transgenic plant according to claim 9, wherein the dicotyledonous plant belongs to the family *Brassicaceae*, *Solanaceae*, *Leguminosae*, *Cucurbitaceae*, *Umbelliferae*, *Asteraceae*, *Malvaceae*, *Chenopodiaceae*, *Myrtaceae*, or *Salicaceae*.

11. A method for imparting salt stress tolerance to plants, wherein the gene according to claim 1 or 2 or the recombinant vector according to claim 3 is introduced into plants.

12. A selection marker for a transgenic plant comprising the gene according to claim 1 or 2.

13. The selection marker for a transgenic plant according to claim 12, wherein the plant is monocotyledonous.

14. The selection marker for a transgenic plant according to claim 13, wherein the monocotyledonous plant belongs to the family *Gramineae*, *Liliaceae*, or *Zingiberaceae*.

15. The selection marker for a transgenic plant according to claim 14, wherein the plant that belongs to the family *Gramineae* is selected from the group consisting of rice, barley, wheat, maize, sugarcane, *Zoysia*, sorghum, Italian millet, and Japanese millet.

16. The selection marker for a transgenic plant according to claim 12, wherein the plant is dicotyledonous.

17. The selection marker for a transgenic plant according to claim 16, wherein

the dicotyledonous plant belongs to the family *Brassicaceae*, *Solanaceae*, *Leguminosae*, *Cucurbitaceae*, *Umbelliferae*, *Asteraceae*, *Malvaceae*, *Chenopodiaceae*, *Myrtaceae*, or *Salicaceae*.

18. A method for selecting a transgenic plant comprising introducing the gene according to claim 1 or 2 or the recombinant vector according to claim 3 into a plant, culturing the plant in galactose-containing medium, and selecting the transgenic plant by employing galactose tolerance as an indicator.